

L3

SEARCH REQUEST FORM

BEST AVAILABLE COPY

Requestor's Name: Karen Behan Carlson Serial Number: 09/902772
 Date: 11-12-02 Phone: 308-0034 Art Unit: 1653
9B01

Search Topic:

Please write a detailed statement of search topic. Describe specifically as possible the subject matter to be searched. Define any terms that may have a special meaning. Give examples or relevant citations, authors keywords, etc., if known. For sequences, please attach a copy of the sequence. You may include a copy of the broadest and/or most relevant claim(s).

(CFS)

Please search and interview
search Ag ID no 1, 2, & 4.

Also nucleic acid encoding
Ag ID no: 2 or no: 4.

Also 645-662 of Ag ID no: 1
and especially primers.

nucl-1-1447

Per 4-478
Rep 2-451

Print out please

Thank you

Karen

Point of Contact:
Barb O'Bryen
Technical Information Specialist
STIC CM1 6A05 308-4291

STAFF USE ONLY

Date completed: 11-12-02Searcher: FBTBTerminal time: 13Elapsed time: over 17CPU-time: Total time: Number of Searches: Number of Databases:

Search Site

 STIC CM-1 Pre-S N.A. Sequence A.A. Sequence Structure Bibliographic

Vendors

 IG Suite STN Dialog APS Geninfo SDC DARC/Questel Other

Dear Examiner,

The attached search was run with the most recently released version of Compugen's search software, GenCore 5. With this update, several changes have occurred in the results of FrameSearches (protein query sequence vs nucleic acid databases or nucleic acid query sequence vs protein databases).

In reference to FrameSearches:

- The output format has been improved so that it more closely resembles the format for standard search output.
- Calculation of Percent Similarity has been changed for FrameSearches. The new method of calculation is more similar to the method used in NCBI's BLAST algorithm. The same results are found in the same order using GenCore 5 and the previous version of GenCore, but Percent Similarities are lower in GenCore 5 results.
 - The formula for % similarity calculation is:

$$100 * \frac{\text{matches} + \text{conservative substitutions}}{\text{alignment_length}}$$

where "matches" is the number of identical matches and "conservative substitutions" is the number of non-identical positive matches.

- GenCore 4.5 considers the match Thr vs GCT (Ala) to be a similarity since BLOSUM62 gives score of 0 to this match. It is marked by '===' in the alignment:

Qy	46	AspSerThrAspAla.Met..Gly	52
		::: :::	
Db	605	GATTCCGCTGCTGCTAATTTGGC	628

GenCore 5 requires a positive score to consider a non-identical match a similarity, therefore the same 'match' is not emphasized in the new alignment:

Qy	46	AspSerThrAspAla.Met..Gly	52
		:::	
Db	605	GATTCCGCTGCTGCTAATTTGGC	628

If you have any questions, please feel free to contact one of the searchers in Biotech/Chem Library.